

SEQUENCE LISTING

<110> DeVico et al, Anthony

<120> VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE

<130> 4115-144 CIP

<160> 33

<170> PatentIn version 3.1

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Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
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Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
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Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
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Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
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Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
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Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
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Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
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Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser
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<212> DNA

<213> Artificial Sequence

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Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
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Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val
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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
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Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys

225		230		235		240
Thr Asn Val Ser	Thr Val Gln Cys	Thr His Gly Ile Arg	Pro Val Val			
	245	250	255			
Ser Thr Gln Leu Leu Leu Asn Gly	Ser Leu Ala Glu Glu Glu Val Val					
	260	265	270			
Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln						
	275	280	285			
Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr						
	290	295	300			
Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly						
305	310	315	320			
Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala						
	325	330	335			
Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln						
	340	345	350			
Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro						
	355	360	365			
Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys						
	370	375	380			
Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser						
	385	390	395	400		
Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys						
	405	410	415			
Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro						
	420	425	430			
Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu						
	435	440	445			
Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg						
	450	455	460			

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly
500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys
515 520 525

Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr
530 535 540

Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln
545 550 555 560

Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser
565 570 575

Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly
580 585 590

Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr
595 600 605

Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val
610 615 620

Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser
625 630 635 640

Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln
645 650 655

Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser
660 665 670

Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val
675 680 685

Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu
690 695 700

Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr
705 710 715 720

<210> 5
<211> 1668
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 5
atgcccatgg ggtctctgca accgctggcc accttgtacc tgctggggat gctggtcgct 60
tcctgcctcg gaaacgccga ggagaagctg tgggtgaccg tgtactacgg cgtgcccgctg 120
tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag 180
gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggaggctg 240
gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggg ggagcagatg 300
cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgcgtgaa gctgaccccc 360
ctgtgcgtga ccctgaactg caccgacctg cgcaacgcc acaacggcaa cgacaccaac 420
accactagta gcagccgcgg catggtggggc ggcgggcgaga tgaagaactg cagcttcaac 480
atcaccacca acatccgcgg caaggtgcag aaggagtacg ccctgttcta caagctggac 540
atcgccccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc 600
gtgatcacc accgctgccc caaggtgagc ttcgagccca tccccatcca ctactgcgcc 660
cccgccggct tcgccatcct gaagtgcaag gacaagaagt tcaacggcaa gggcccctgc 720
accaacgtga gcaccgtgca gtgcaccac ggcacccgcc ccgtgggtgag caccagctg 780
ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgccaa cttcgccgac 840
aacgccaagg tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcccc 900
aacaacaaca cccgcaagtc catccacatc ggccccggcc gcgccttcta caccaccggc 960
gagatcatcg gcgacatccg ccaggcccac tgcaacctga gccgcgccaa gtggaacgac 1020
accctgaaca agatcgtgat caagctgctg gagcagttcg gcaacaagac catcgtgttc 1080
aagcacagca gcggcggcga ccccgagatc gtgaccacaca gcttcaattg cggcgggcag 1140
ttcttctact gcaacagcac ccagctgttc aacagcacct ggaacgtgac cgaggagagc 1200

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aacaacaccg tggagaacaa caccatcacc ctgccctgcc gcatcaagca gatcatcaac 1260
atgtggcagg aggtggggccg cgccatgtac gcccccccca tccgcgccca gatccgctgc 1320
agttchaaca tcaccggcct gctgctgacc cgcgacggcg gccccgagga caacaagacc 1380
gaggtgttcc gccccggcgg cggcgacatg cgcgacaact ggcgcagcga gctgtacaag 1440
tacaaggtgg tgaagatcga gccctggggc gtggccccca ccaaggccaa gcgcgcgtg 1500
gtgcagcgcg agaagaccgg atcctctggt ggcggtggct cgggctccgg aggaggtggg 1560
tcgggtggcg gcgcggccgc ttgcaacctg gcccgctgcc agctgcgctg caagagcctg 1620
ggcctgctgg gcaagtgcgc cggcagcttc tgcgcctgcg gcccctaa 1668

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<210> 6
<211> 556
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthesized construct

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<220>
<221> MISC_FEATURE
<222> (1)..(556)
<223> X can be any amino acid

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<400> 6

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Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
1          5          10          15

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Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val
          20          25          30

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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
          35          40          45

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Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
          50          55          60

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Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65          70          75          80

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Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
          85          90          95

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Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln
275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala
 325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln
 340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro
 355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
 385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
 405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
 420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
 435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
 450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
 465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
 485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly
 500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Cys
 515 520 525

Asn Leu Ala Arg Cys Gln Leu Arg Cys Lys Ser Leu Gly Leu Leu Gly
 530 535 540

Lys Cys Ala Gly Ser Phe Cys Ala Cys Gly Pro Xaa

545

550

555

<210> 7
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized construct

<220>
 <221> primer
 <222> (1)..(39)
 <223>

<400> 7
 ggggggtacca tgcccatggg gtctctgcaa ccgctggcc 39

<210> 8
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized construct

<400> 8
 ggggtccggag cccgagccac cgccaccaga ggatccacgc ttctcgcgct gcaccacgcg 60

gcgctt 66

<210> 9
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized construct

<220>
 <221> primer
 <222> (1)..(69)
 <223>

<400> 9
 ggggtccggag gaggtgggtc ggggtggcggc gcggccgcta agaaagtggg gctggggcaaa 60

aaaggggat 69

<210> 10
 <211> 76

<212> DNA
 <213> Artificial Sequence

<220>
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<220>
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 <222> (1)..(76)
 <223>

<400> 10
 ggggttttaa cttattacag atcctcttct gagatgagtt ttgttcagct agcaccacga 60
 tgtctatttt gaactc 76

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized construct

<220>
 <221> spacer
 <222> (1)..(21)
 <223>

<400> 11
 gssggggsgs gggsggggaa a 21

<210> 12
 <211> 1769
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized construct

<400> 12
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 cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 180
 acccccctgt gcgtgaccct gggcgcgggc gagatgaaga actgcagctt caacatcggc 240
 gcgggcccgc tgatcagctg caacaccagc gtgatcacc aggctgccc caaggtgagc 300
 ttcgagccca tccccatcca ctactgcgc cccgcgggct tcgccatcct gaagtgaag 360

<220>
 <221> MISC_FEATURE
 <222> (1)..(590)
 <223> X can be any amino acid

<400> 13

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
 1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Lys Asn Val Thr Glu Asn Phe Asn
 20 25 30

Met Trp Lys Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser
 35 40 45

Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys
 50 55 60

Val Thr Leu Gly Ala Gly Glu Met Lys Asn Cys Ser Phe Asn Ile Gly
 65 70 75 80

Ala Gly Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys
 85 90 95

Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
 100 105 110

Gly Phe Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly
 115 120 125

Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro
 130 135 140

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu
 145 150 155 160

Val Val Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile
 165 170 175

Val Gln Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn
 180 185 190

Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr

195

200

205

Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser
 210 215 220

Arg Ala Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg
 225 230 235 240

Glu Gln Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly
 245 250 255

Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe
 260 265 270

Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu
 275 280 285

Glu Ser Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg
 290 295 300

Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr
 305 310 315 320

Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly
 325 330 335

Leu Leu Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val
 340 345 350

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu
 355 360 365

Tyr Lys Tyr Lys Val Val Lys Ile Gly Ser Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys Lys Val
 385 390 395 400

Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser
 405 410 415

Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys
 420 425 430

Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu
435 440 445

Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe
450 455 460

Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile
465 470 475 480

Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly
485 490 495

Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr
500 505 510

Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg
515 520 525

Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser
530 535 540

Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln
545 550 555 560

Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Glu
565 570 575

Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr
580 585 590

<210> 14

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> MISC_FEATURE

<222> (1)..(15)

<223> X can be any amino acid

<400> 14

Sequence = 334660

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr
1 5 10 15

<210> 15
<211> 111
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 15
gggggtacca tgcccatggg gtctctgcaa ccgctggcca ccttgtagct gctggggatg 60
ctgggtcgctt cctgcctcgg aaagaacgtg accgagaact tcaacatgtg g 111

<210> 16
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 16
gggggatccg atcttcacca ccttgatctt gtacagctc 39

<210> 17
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 17
ctgtgcgtga ccctgggagc ggccgagatg aagaactgca gcttcaacat cggcgcgggc 60
cgccatgatca gctgc 75

<210> 18
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 18
gcagctgac aggcggcccg cgccgatgtt gaagctgcag ttcttcatct cgcccgcgcc 60
cagggtcacg cacag 75

<210> 19
 <211> 87
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized construct

 <400> 19
 tgcaacctgg ccgctgccca gctgcgctgc aagagcctgg gcctgctggg caagtgcgcc 60
 ggcagcttct gcgcctgcgg cccctaa 87

<210> 20
 <211> 28
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthesized construct

 <400> 20
 Cys Asn Leu Ala Arg Cys Gln Leu Arg Cys Lys Ser Leu Gly Leu Leu
 1 5 10 15
 Gly Lys Cys Ala Gly Ser Phe Cys Ala Cys Gly Pro
 20 25

<210> 21
 <211> 102
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized construct

 <400> 21
 gcggccgctt gcaacctggc ccgctgccag ctgcgctgca agagcctggg cctgctgggc 60
 aagtgcgccg gcagcttctg cgctgcggc ccctaagaat tc 102

<210> 22
 <211> 102
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthesized construct

 <400> 22

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gaattcttag gggccgcagg cgcagaagct gccggcgcac ttgccagca ggcccaggct      60
cttgacgcgc agctggcagc gggccagggt gcaagcggcc gc                        102

<210> 23
<211> 1518
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 23
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tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag      180
gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagggtg      240
gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggt ggagcagatg      300
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atcgccccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc      600
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ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgccaa cttcgccgac      840
aacgccaagg tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcccc      900
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gagatcatcg gcgacatccg ccaggccccc tgcaacctga gccgcgcca gtggaacgac      1020
accctgaaca agatcgtgat caagctgcgc gagcagttcg gcaacaagac catcgtgttc      1080
aagcacagca gcggcggcga ccccgagatc gtgaccacaa gcttcaattg cggcgggcgag      1140
ttcttctact gcaacagcac ccagctgttc aacagcacct ggaacgtgac cgaggagagc      1200
aacaacaccg tggagaacaa caccatcacc ctgccctgcc gcatcaagca gatcatcaac      1260
atgtggcagg aggtggggcg cgccatgtac gccccccca tccgcggcc gatccgctgc      1320

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agttchaaca tcaccggcct gctgctgacc cgcgacggcg gccccgagga caacaagacc 1380
gaggtgttcc gccccggcgg cggcgacatg cgcgacaact ggcgcagcga gctgtacaag 1440
tacaagggtgg tgaagatcga gcccctgggc gtggccccc ccaaggccaa gcgccgcgtg 1500
gtgcagcgcg agaagcgt 1518

<210> 24
<211> 506
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthesized construct
<400> 24

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val
20 25 30

Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn

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145	150	155	160
Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe	165	170	175
Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr	180	185	190
Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys	195	200	205
Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe	210	215	220
Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys	225	230	235
Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val	245	250	255
Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val	260	265	270
Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln	275	280	285
Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr	290	295	300
Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly	305	310	315
Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala	325	330	335
Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln	340	345	350
Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro	355	360	365
Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys	370	375	380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Arg
500 505

<210> 25
<211> 534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 25
aagaaagtgg tgctgggcaa aaaaggggat acagtggaac tgacctgtac agcttcccag 60
aagaagagca tacaattcca ctggaaaaac tccaaccaga taaagattct gggaaatcag 120
ggctccttct taactaaagg tccatccaag ctgaatgac gcgctgactc aagaagaagc 180
ctttgggacc aaggaaactt cccctgac atcaagaatc ttaagataga agactcagat 240
acttacatct gtgaagtgga ggaccagaag gaggaggtgc aattgctagt gttcggattg 300
actgccaaact ctgacaccca cctgcttcag gggcagagcc tgaccctgac cttggagagc 360
cccctggta gtagccctc agtgcaatgt aggagtccaa ggggtaaaaa catacagggg 420

gggaagaccc tctccgtgtc tcagctggag ctccaggata gtggcacctg gacatgcact 480
gtcttgcaga accagaagaa ggtggagttc aaaatagaca tcgtggtgct agct 534

<210> 26
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 26

Lys Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys
1 5 10 15

Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn
20 25 30

Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro
35 40 45

Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln
50 55 60

Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp
65 70 75 80

Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu
85 90 95

Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln
100 105 110

Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val
115 120 125

Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu
130 135 140

Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr
145 150 155 160

Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val
165 170 175

Leu Ala

<210> 27
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized construct

<400> 27
atgcccatgg ggtctctgca accgctggcc accttgtacc tgctggggat gctggtcgct 60
tcctgcctcg gaaagaacgt gaccgagaac ttcaacatgt ggaagaacaa catggtggag 120
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 180
acccccctgt gcgtgaccct gggcgcgggc gagatgaaga actgcagctt caacatcggc 240
gcggggccgcc tgatcagctg caacaccagc gtgatcacc aggcctgccc caaggtgagc 300
ttcagagcca tccccatcca ctactgcgc cccgcgggt tcgccatcct gaagtgaag 360
gacaagaagt tcaacggcaa gggccccctgc accaacgtga gcaccgtgca gtgcaccac 420
ggcatccgcc ccgtgggtgag caccagctg ctgctgaacg gcagcctggc cgaggaggag 480
gtgggtgatcc gcagcgccaa cttcgccgac aacgccaagg tgatcatcgt gcagctgaac 540
gagagcgtgg agatcaactg caccgcccc aacaacaaca cccgcaagtc catccacatc 600
ggccccggcc gcgccttcta caccaccggc gagatcatcg gcgacatccg ccaggccac 660
tgcaacctga gccgcgcaa gtggaacgac accctgaaca agatcgtgat caagctgcgc 720
gagcagttcg gcaacaagac catcgtgttc aagcacagca gcggcggcga ccccgagatc 780
gtgaccaca gttcaattg cggcggcgag ttcttctact gcaacagcac ccagctgttc 840
aacagcacct ggaacgtgac cgaggagagc aacaacaccg tggagaacaa caccatcacc 900
ctgccctgcc gcatcaagca gatcatcaac atgtggcagg aggtggggcg cgccatgtac 960
gcccccccca tccgcggcca gatccgctgc agttchaaca tcaccggcct gctgctgacc 1020
cgcgacggcg gccccgagga caacaagacc gaggtgttcc gccccggcg cggcgacatg 1080
cgcgacaact ggcgcagcga gctgtacaag tacaagggtg tgaagatc 1128

<210> 28
<211> 376
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 28

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Lys Asn Val Thr Glu Asn Phe Asn
20 25 30

Met Trp Lys Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser
35 40 45

Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys
50 55 60

Val Thr Leu Gly Ala Gly Glu Met Lys Asn Cys Ser Phe Asn Ile Gly
65 70 75 80

Ala Gly Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys
85 90 95

Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
100 105 110

Gly Phe Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly
115 120 125

Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro
130 135 140

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu
145 150 155 160

Val Val Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile
165 170 175

Val Gln Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn
180 185 190

Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr
195 200 205

Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser
 210 215 220

Arg Ala Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg
 225 230 235 240

Glu Gln Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly
 245 250 255

Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe
 260 265 270

Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu
 275 280 285

Glu Ser Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg
 290 295 300

Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr
 305 310 315 320

Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly
 325 330 335

Leu Leu Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val
 340 345 350

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu
 355 360 365

Tyr Lys Tyr Lys Val Val Lys Ile
 370 375

<210> 29

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized construct

<400> 29

atgccccatgg ggtctctgca accgctggcc acctgtacc tgctggggat gctggtcgct

60

tcctgcctcg gaaacgccga ggagaagctg tgggtgaccg tgtactacgg cgtgcccgtg 120
 tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag 180
 gtgcacaacg tgtggggcac ccacgcctgc gtgcccaccg accccaaccc ccaggaggtg 240
 gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggt ggagcagatg 300
 cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgcgtgaa gctgaccccc 360
 ctgtgcgtga ccctgaactg caccgacctg cgcaacgcc acaacggcaa cgacaccaac 420
 accactagta gcagccgcgg catggtgggc ggcggcgaga tgaagaactg cagcttcaac 480
 atcaccacca acatccgcgg caaggtgcag aaggagtacg ccctgttcta caagctggac 540
 atcgccccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc 600
 gtgatcacc aggcctgccc caaggtgagc ttcgagccca tccccatcca ctactgcgcc 660
 cccgccggct tcgccatcct gaagtgcagg gacaagaagt tcaacggcaa gggcccctgc 720
 accaacgtga gcaccgtgca gtgcacccac ggcacccgcc ccgtgggtgag caccagctg 780
 ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgccaa cttcgccgac 840
 aacgccaagg tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcccc 900
 aacaacaaca cccgcaagtc catccacatc ggcgccggcc gcgccttcta caccaccggc 960
 gagatcatcg gcgacatccg ccaggccccc tgcaacctga gccgcgccaa gtggaacgac 1020
 accctgaaca agatcgtgat caagctgcgc gagcagttcg gcaacaagac catcgtgttc 1080
 aagcacagca gcggcggcga ccccgagatc gtgaccacaa gcttcaattg cggcggcgag 1140
 ttcttctact gcaacagcac ccagctgttc aacagcacct ggaacgtgac cgaggagagc 1200
 aacaacaccg tggagaacaa caccatcacc ctgccctgcc gcatcaagca gatcatcaac 1260
 atgtggcagg aggtggggcg cgccatgtac gccccccca tccgcggcca gatccgctgc 1320
 agttchaaca tcaccggcct gctgctgacc cgcgacggcg gcccgcagga caacaagacc 1380
 gaggtgttcc gcccgcggcg cggcgacatg cgcgacaact ggcgacagca gctgtacaag 1440
 tacaaggtgg tgaagatcga gccctgggc gtggccccc acaaggccaa gcgccgcgtg 1500
 gtgcagcgcg agaagacc 1518

<210> 30
 <211> 506
 <212> PRT
 <213> Artificial Sequence
 <220>

<223> Synthesized construct

<400> 30

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val
20 25 30

Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe

210

215

220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys
 225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
 245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
 260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln
 275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
 290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly
 305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala
 325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln
 340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro
 355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys
 370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser
 385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys
 405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
 420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
 435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg
 450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
 465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala
 485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr
 500 505

<210> 31
 <211> 776
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized construct

<400> 31
 atgcccatgg ggtctctgca accgctggcc accttgtacc tgctggggat gctggtcgct 60
 tccgtgctag cggatcccca ggagcccaaa tcttgtgaca aaactcacac atgccaccg 120
 tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaacccaag 180
 gacaccctca tgatctcccg gaccctgag gtcacatgcg tgggtggtgga cgtgagccac 240
 gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaaag 300
 acaaagccgc gggaggagca gtacaacagc acgtaccggg tggtcagcgt cctcaccgtc 360
 ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc 420
 ccagcccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacagggtg 480
 tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 540
 gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 600
 aacaactaca agaccagcc tcccgctgctg gactccgacg gctccttctt cctctacagc 660
 aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 720
 catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaa 776

<210> 32
 <211> 259
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> MISC_FEATURE

<222> (1)..(259)

<223> X is any amino acid

<400> 32

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
1 5 10 15

Met Leu Val Ala Ser Val Leu Ala Asp Pro Glu Glu Pro Lys Ser Cys
20 25 30

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
35 40 45

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
50 55 60

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
65 70 75 80

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
85 90 95

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
100 105 110

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
115 120 125

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
130 135 140

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
145 150 155 160

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
165 170 175

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 180 185 190

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 195 200 205

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 210 215 220

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 225 230 235 240

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 245 250 255

Pro Gly Xaa

<210> 33
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized construct

<400> 33
 ggatcctctg gtggcgggtgg ctcgggctcc ggaggaggtg ggtcgggtgg cggcgcggcc 60
 gct 63